

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10 | 784,721
Source: IFW0
Date Processed by STIC: 11/17/2005

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 11/17/2005

PATENT APPLICATION: US/10/784,721

TIME: 09:55:15

Input Set : N:\Crif3\RULE60\10784721.raw

Output Set: N:\CRF4\11172005\J784721.raw

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1 <110> APPLICANT: Muir, Tom
2      Cotton, Graham
3      The Rockefeller University
4 <120> TITLE OF INVENTION: Multiple Sensor-Containing Polypeptides,
5      Methods of Preparation and Uses Thereof
6 <130> FILE REFERENCE: RU 453
7 <140> CURRENT APPLICATION NUMBER: US/10/784,721
8 <141> CURRENT FILING DATE: 2004-02-23
9 <150> PRIOR APPLICATION NUMBER: US/09/483,543
10 <151> PRIOR FILING DATE: 2000-01-14
11 <160> NUMBER OF SEQ ID NOS: 10
12 <170> SOFTWARE: FastSEQ for Windows Version 3.0
14 <210> SEQ ID NO: 1
15 <211> LENGTH: 8
16 <212> TYPE: PRT
17 <213> ORGANISM: Artificial Sequence
18 <220> FEATURE:
19 <223> OTHER INFORMATION: Cleavage Site for PreScission Protease
20 <400> SEQUENCE: 1
21      Leu Glu Val Leu Phe Gln Gly Pro
22      1          5
24 <210> SEQ ID NO: 2
25 <211> LENGTH: 12
26 <212> TYPE: PRT
27 <213> ORGANISM: Artificial Sequence
28 <220> FEATURE:
29 <223> OTHER INFORMATION: Peptide Substrate
30 <400> SEQUENCE: 2
31      Glu Ala Ile Tyr Ala Ala Pro Phe Ala Lys Lys Lys
32      1          5          10
34 <210> SEQ ID NO: 3
35 <211> LENGTH: 64
36 <212> TYPE: DNA
37 <213> ORGANISM: Artificial Sequence
38 <220> FEATURE:
39 <223> OTHER INFORMATION: Primer
40 <400> SEQUENCE: 3
41      aaaagaaaaa aaggcggccg ctcggatctg atcgaagggtc gttgtgcggg caacttcgac
42      tcgg
44 <210> SEQ ID NO: 4
45 <211> LENGTH: 40
46 <212> TYPE: DNA
47 <213> ORGANISM: Artificial Sequence

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48 <220> FEATURE:
49 <223> OTHER INFORMATION: Primer
50 <400> SEQUENCE: 4
51      gcaaaactggc tcttccgcag ccgctgaagt cctcatcggg
53 <210> SEQ ID NO: 5
54 <211> LENGTH: 18
55 <212> TYPE: PRT
56 <213> ORGANISM: Artificial Sequence
57 <220> FEATURE:
58 <223> OTHER INFORMATION: Xa-Cys- (Crk-II)-Intein-CBD Construct
59 <400> SEQUENCE: 5
60      Met Ala Ser Ser Arg Val Asp Gly Gly Arg Ser Asp Leu Ile Glu Gly
61      1              5              10              15
62      Arg Cys
64 <210> SEQ ID NO: 6
65 <211> LENGTH: 18
66 <212> TYPE: PRT
67 <213> ORGANISM: Artificial Sequence
68 <220> FEATURE:
69 <223> OTHER INFORMATION: Cys-F1-PS-Biotin Construct
70 <220> FEATURE:
71 <221> NAME/KEY: misc_feature
72 <222> LOCATION: 3
73 <223> OTHER INFORMATION: Xaa = Lys-[Dapa(F1)]
74 <220> FEATURE:
75 <221> NAME/KEY: misc_feature
76 <222> LOCATION: 17
77 <223> OTHER INFORMATION: Xaa = [Lys-(Biotin)]
78 <400> SEQUENCE: 6
W--> 79      Cys Gly Xaa Gly Leu Glu Val Leu Phe Gln Gly Pro Val Arg Lys Gly
80      1              5              10              15
W--> 81      Xaa Gly
83 <210> SEQ ID NO: 7
84 <211> LENGTH: 11
85 <212> TYPE: PRT
86 <213> ORGANISM: Artificial Sequence
87 <220> FEATURE:
88 <223> OTHER INFORMATION: High affinity ligand for the N-SH3 Domain of Crk
89 <400> SEQUENCE: 7
90      Pro Pro Pro Ala Leu Pro Pro Lys Arg Arg Arg
91      1              5              10
93 <210> SEQ ID NO: 8
94 <211> LENGTH: 318
95 <212> TYPE: PRT
96 <213> ORGANISM: Artificial Sequence
97 <220> FEATURE:
98 <223> OTHER INFORMATION: Protein Kinase Target
99 <220> FEATURE:
100 <221> NAME/KEY: misc_feature

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101 <222> LOCATION: 311

102 <223> OTHER INFORMATION: Xaa = Lys-[Dapa(Fl)]

103 <400> SEQUENCE: 8

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104   Lys Arg Gly Cys Ala Gly Asn Phe Asp Ser Glu Glu Arg Ser Ser Trp
105       1           5           10           15
106   Tyr Trp Gly Arg Leu Ser Arg Gln Glu Ala Val Ala Leu Leu Gln Gly
107           20           25           30
108   Gln Arg His Gly Val Phe Leu Val Arg Asp Ser Ser Thr Ser Pro Gly
109           35           40           45
110   Asp Tyr Val Leu Ser Val Ser Glu Asn Ser Arg Val Ser His Tyr Ile
111           50           55           60
112   Ile Asn Ser Ser Gly Pro Arg Pro Pro Val Pro Pro Ser Pro Ala Gln
113           65           70           75           80
114   Pro Pro Pro Gly Val Ser Pro Ser Arg Leu Arg Ile Gly Asp Gln Glu
115           85           90           95
116   Phe Asp Ser Leu Pro Ala Leu Leu Glu Phe Tyr Lys Ile His Tyr Leu
117           100          105          110
118   Asp Thr Thr Thr Leu Ile Glu Pro Val Ala Arg Ser Arg Gln Gly Ser
119           115          120          125
120   Gly Val Ile Leu Arg Gln Glu Glu Ala Glu Tyr Val Arg Ala Leu Phe
121           130          135          140
122   Asp Phe Asn Gly Asn Asp Glu Glu Asp Leu Pro Phe Lys Lys Gly Asp
123           145          150          155          160
124   Ile Leu Arg Ile Arg Asp Lys Pro Glu Glu Gln Trp Trp Asn Ala Glu
125           165          170          175
126   Asp Ser Glu Gly Lys Arg Gly Met Ile Pro Val Pro Tyr Val Glu Lys
127           180          185          190
128   Tyr Arg Pro Ala Ser Ala Ser Val Ser Ala Leu Ile Gly Gly Asn Gln
129           195          200          205
130   Glu Gly Ser His Pro Gln Pro Leu Gly Gly Pro Glu Pro Gly Pro Tyr
131           210          215          220
132   Ala Gln Pro Ser Val Asn Thr Pro Leu Pro Asn Leu Gln Asn Gly Pro
133           225          230          235          240
134   Ile Tyr Ala Arg Val Ile Gln Lys Arg Val Pro Asn Ala Tyr Asp Lys
135           245          250          255
136   Thr Ala Leu Ala Leu Glu Val Gly Glu Leu Val Lys Val Thr Lys Ile
137           260          265          270
138   Asn Val Ser Gly Gln Trp Glu Gly Glu Cys Asn Gly Lys Arg Gly His
139           275          280          285
140   Phe Pro Phe Thr His Val Arg Leu Leu Asp Gln Gln Asn Pro Asp Glu
141           290          295          300
W--> 142   Asp Phe Ser Gly Cys Gly Xaa Gly Leu Glu Val Leu Phe Gln
143           305          310          315

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145 <210> SEQ ID NO: 9

146 <211> LENGTH: 326

147 <212> TYPE: PRT

148 <213> ORGANISM: Artificial Sequence

149 <220> FEATURE:

150 <223> OTHER INFORMATION: Recombinant Intermediate

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151 <220> FEATURE:
152 <221> NAME/KEY: misc_feature
153 <222> LOCATION: 311
154 <223> OTHER INFORMATION: Xaa = Lys-[Dapa(Fl)]
155 <220> FEATURE:
156 <221> NAME/KEY: misc_feature
157 <222> LOCATION: 325
158 <223> OTHER INFORMATION: Xaa = [Lys-(Biotin)]
159 <400> SEQUENCE: 9
160     Lys Arg Gly Cys Ala Gly Asn Phe Asp Ser Glu Glu Arg Ser Ser Trp
161         1             5             10             15
162     Tyr Trp Gly Arg Leu Ser Arg Gln Glu Ala Val Ala Leu Leu Gln Gly
163         20             25             30
164     Gln Arg His Gly Val Phe Leu Val Arg Asp Ser Ser Thr Ser Pro Gly
165         35             40             45
166     Asp Tyr Val Leu Ser Val Ser Glu Asn Ser Arg Val Ser His Tyr Ile
167         50             55             60
168     Ile Asn Ser Ser Gly Pro Arg Pro Pro Val Pro Ser Pro Ala Gln
169         65             70             75             80
170     Pro Pro Pro Gly Val Ser Pro Ser Arg Leu Arg Ile Gly Asp Gln Glu
171         85             90             95
172     Phe Asp Ser Leu Pro Ala Leu Leu Glu Phe Tyr Lys Ile His Tyr Leu
173         100            105            110
174     Asp Thr Thr Thr Leu Ile Glu Pro Val Ala Arg Ser Arg Gln Gly Ser
175         115            120            125
176     Gly Val Ile Leu Arg Gln Glu Glu Ala Glu Tyr Val Arg Ala Leu Phe
177         130            135            140
178     Asp Phe Asn Gly Asn Asp Glu Glu Asp Leu Pro Phe Lys Lys Gly Asp
179         145            150            155            160
180     Ile Leu Arg Ile Arg Asp Lys Pro Glu Glu Gln Trp Trp Asn Ala Glu
181         165            170            175
182     Asp Ser Glu Gly Lys Arg Gly Met Ile Pro Val Pro Tyr Val Glu Lys
183         180            185            190
184     Tyr Arg Pro Ala Ser Ala Ser Val Ser Ala Leu Ile Gly Gly Asn Gln
185         195            200            205
186     Glu Gly Ser His Pro Gln Pro Leu Gly Gly Pro Glu Pro Gly Pro Tyr
187         210            215            220
188     Ala Gln Pro Ser Val Asn Thr Pro Leu Pro Asn Leu Gln Asn Gly Pro
189         225            230            235            240
190     Ile Tyr Ala Arg Val Ile Gln Lys Arg Val Pro Asn Ala Tyr Asp Lys
191         245            250            255
192     Thr Ala Leu Ala Leu Glu Val Gly Glu Leu Val Lys Val Thr Lys Ile
193         260            265            270
194     Asn Val Ser Gly Gln Trp Glu Gly Glu Cys Asn Gly Lys Arg Gly His
195         275            280            285
196     Phe Pro Phe Thr His Val Arg Leu Leu Asp Gln Gln Asn Pro Asp Glu
197         290            295            300
W--> 198     Asp Phe Ser Gly Cys Gly Xaa Gly Leu Glu Val Leu Phe Gln Gly Pro
199         305            310            315            320

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Input Set : N:\Crf3\RULE60\10784721.raw

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W--> 200 Val Arg Lys Gly Xaa Gly
201 325
203 <210> SEQ ID NO: 10
204 <211> LENGTH: 5
205 <212> TYPE: PRT
206 <213> ORGANISM: Artificial Sequence
207 <220> FEATURE:
208 <223> OTHER INFORMATION: Site for Sequential Ligation
209 <220> FEATURE:
210 <221> NAME/KEY: misc_feature
211 <222> LOCATION: 5
212 <223> OTHER INFORMATION: Xaa = Cys (Xa-Cys)
213 <400> SEQUENCE: 10
W--> 214 Ile Glu Gly Arg Xaa
215 1 5

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/784,721

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Input Set : N:\Crf3\RULE60\10784721.raw
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:6; Xaa Pos. 3,17
Seq#:8; Xaa Pos. 311
Seq#:9; Xaa Pos. 311,325
Seq#:10; Xaa Pos. 5

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:3; Line(s) 41,42
Seq#:4; Line(s) 51

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10784721.raw

Output Set: N:\CRF4\11172005\J784721.raw

L:79 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:81 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:16
L:142 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:304
L:198 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:304
L:200 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:320
L:214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0